

SEQUENCE LISTING

<110> Braun, Jonathan
Sutton, Christopher L.

<120> IBD-Associated Microbial Nucleic Acid
Molecules

<130> P-PM 4966

<150> US 09/303,120

<151> 1999-04-30

<150> US 09/820,576

<151> 2001-03-28

<160> 10

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 302

<212> DNA

<213> Unknown

<220>

<223> Microbial Organism from the human gut

<221> CDS

<222> (2)...(301)

<400> 1

a gat ctg gcc agc gcc qtg ggc atc cag tcc ggc agc atc ttt cat cac 49
Asp Leu Ala Ser Ala Val Gly Ile Gln Ser Gly Ser Ile Phe His His
1 5 10 15

ttc aag agc aag gat gag ata ttg cgt gcc gtg atg gag gaa acc atc 97
Phe Lys Ser Lys Asp Glu Ile Leu Arg Ala Val Met Glu Glu Thr Ile
8 20 25 30

cat tac aac acc gcg atg atg cgc gct tca ctg gag gag gcg agc acg 145
His Tyr Asn Thr Ala Met Met Arg Ala Ser Leu Glu Ala Ser Thr
35 40 45

gtg cgc gaa cgc gtg ctg gcg atc cgc tgc gag ttg cag tcg atc 193
Val Arg Glu Arg Val Leu Ala Leu Ile Arg Cys Glu Leu Gln Ser Ile
50 55 60

atg ggc ggc agt ggc gag gcc atg gcg gtg ctg gtc tac gaa tgg cgc 241
Met Gly Gly Ser Gly Glu Ala Met Ala Val Leu Val Tyr Glu Trp Arg
65 70 75 80



tcg ctg tcg gcc gaa ggc cag gcg cac gtg ctg gcc ctg cgt gac gtg 289
Ser Leu Ser Ala Glu Gly-Gln Ala His Val Leu Ala Leu Arg Asp Val
85 (5) 90 95

tat gag cag atc t 302
Tyr Glu Gln Ile
100

<210> 2
<211> 100
<212> PRT
<213> Unknown

<220>
<223> Microbial organism from the human gut

<400> 2
Asp Leu Ala Ser Ala Val Gly Ile Gln Ser Gly Ser Ile Phe His His
1 5 10 15
Phe Lys Ser Lys Asp Glu Ile Leu Arg Ala Val Met Glu Glu Thr Ile
20 25 30
His Tyr Asn Thr Ala Met Met Arg Ala Ser Leu Glu Glu Ala Ser Thr
35 40 45
Val Arg Glu Arg Val Leu Ala Leu Ile Arg Cys Glu Leu Gln Ser Ile
50 55 60
Met Gly Gly Ser Gly Glu Ala Met Ala Val Leu Val Tyr Glu Trp Arg
65 70 75 80
Ser Leu Ser Ala Glu Gly Gln Ala His Val Leu Ala Leu Arg Asp Val
85 90 95
Tyr Glu Gln Ile
100

<210> 3
<211> 392
<212> DNA
<213> Unknown

<220>
<223> Microbial Organism from the human gut

<221> CDS
<222> (2)...(346)

<221> misc_feature
<222> (1)...(392)
<223> n = A,T,C or G

<400> 3
a gat ctt gag cgt cat gag tgc ctg ggg tac gcc ttt tca tcg cgt ccg 49
Asp Leu Glu Arg His Glu Cys Leu Gly Tyr Ala Phe Ser Ser Arg Pro
1 5 10 15

gct gat cga gag tgg gtg ttt ttt cag ggc acg gtt tcc tac aag gta 97
Ala Asp Arg Glu Trp Val Phe Phe Gln Gly Thr Val Ser Tyr Lys Val
20 25 30

cga gtg gcc agc cgt ttg ctc atc aat gaa agc cgg gca ttg atg tcg 145
Arg Val Ala Ser Arg Leu Leu Ile Asn Glu Ser Arg Ala Leu Met Ser
35 40 45

gct gca ttg gat ggt ttt ggc ata gtg ctc ggc cgg caa gac ttc ctg 193
Ala Ala Leu Asp Gly Phe Gly Ile Val Leu Gly Pro Gln Asp Phe Leu
50 55 60

cga acg gct ttg gct agt ggc gag ttg gtg cgg gtg ttg ccg gag ttt 241
Arg Thr Ala Leu Ala Ser Gly Glu Leu Val Arg Val Leu Pro Glu Phe
65 70 75 80

gag gct ccg agt cgg tcg atg cat ttg gtc tac acc gca aac cgc cag 289
Glu Ala Pro Ser Arg Ser Met His Leu Val Tyr Thr Ala Asn Arg Gln
85 90 95

cgt acc gcc aag ttg cgc tgc ttt gtc gag act gtg ctg gga cgt ttt 337
Arg Thr Ala Lys Leu Arg Cys Phe Val Glu Thr Val Leu Gly Arg Phe
100 105 110

ggc ccg gta tgaaggagca ccaccgtggc ggtcgccggg angcacctaa 386
Gly Pro Val
115

agatct 392

<210> 4
<211> 115
<212> PRT
<213> Unknown

<220>
<223> Microbial organism from the human gut

<400> 4
Asp Leu Glu Arg His Glu Cys Leu Gly Tyr Ala Phe Ser Ser Arg Pro
1 5 10 15
Ala Asp Arg Glu Trp Val Phe Phe Gln Gly Thr Val Ser Tyr Lys Val
20 25 30
Arg Val Ala Ser Arg Leu Leu Ile Asn Glu Ser Arg Ala Leu Met Ser
35 40 45
Ala Ala Leu Asp Gly Phe Gly Ile Val Leu Gly Pro Gln Asp Phe Leu
50 55 60
Arg Thr Ala Leu Ala Ser Gly Glu Leu Val Arg Val Leu Pro Glu Phe
65 70 75 80
Glu Ala Pro Ser Arg Ser Met His Leu Val Tyr Thr Ala Asn Arg Gln
85 90 95
Arg Thr Ala Lys Leu Arg Cys Phe Val Glu Thr Val Leu Gly Arg Phe

100 105 110
Gly Pro Val
115

<210> 5
<211> 114
<212> PRT
<213> Unknown

<220>
<223> Microbial Organism from the human gut

<221> VARIANT
<222> (1)...(114)
<223> Xaa = Any Amino Acid

<400> 5
Arg Thr Arg Arg Ile Ser Leu Pro His Lys Lys Leu Ala Arg Asn Gly
1 5 10 15
Val Leu Tyr Ser His Gly Ala Thr Gln Glu Asp Ile Phe Ala Pro Cys
20 25 30
Gln His Arg Arg Cys Gln Ile Thr Lys Ala Tyr His Glu Ala Arg Leu
35 40 45
Val Glu Gln Ser Arg Arg Gln Arg Thr Ala Leu Gln His Pro His Gln
50 55 60
Arg Leu Lys Leu Ser Arg Thr Pro Arg His Met Gln Asp Val Gly Cys
65 70 75 80
Val Ala Leu Thr Gly Gly Leu Gln Ala Ala Lys Asp Leu Ser His Gln
85 90 95
Ser Thr Lys Thr Arg Tyr Ser Pro Ala Gly Gly His Arg Asp Gly Pro
100 105 110
Xaa Val

<210> 6
<211> 190
<212> PRT
<213> Clostridium pasteurianum

<400> 6
Met Asn Lys Thr Lys Asp Asn Ile Phe Tyr Ser Ala Ile Lys Val Phe
1 5 10 15
Ser Asn Asn Gly Tyr Asn Gly Ala Thr Met Asp Glu Ile Ala Ser Asn
20 25 30
Ala Gly Val Ala Lys Gly Thr Leu Tyr Tyr His Phe Lys Ser Lys Glu
35 40 45
Glu Ile Phe Lys Tyr Ile Ile Glu Glu Gly Val Asn Leu Met Lys Asn
50 55 60
Glu Ile Asp Glu Ala Thr Asp Lys Glu Lys Thr Ala Leu Glu Lys Leu
65 70 75 80
Lys Ala Val Cys Arg Val Gln Leu Asn Leu Ile Tyr Lys Asn Arg Asp

	85	90	95
Phe Phe Lys Val Ile Ala Ser Gln Leu Trp Gly Lys Glu Leu Arg Gln			
100	105	110	
Leu Glu Leu Arg Asp Ile Met Arg Asn Tyr Val Val His Ile Glu Glu			
115	120	125	
Phe Val Lys Asp Ala Met Glu Ala Gly Ser Ile Lys Lys Gly Asn Ser			
130	135	140	
Leu Phe Val Ala Tyr Ala Phe Leu Gly Thr Leu Cys Ser Val Ser Leu			
145	150	155	160
Tyr Glu Val Ile Asn Ala Glu Asn Asp Asn Ile Asn Asn Thr Ile Glu			
165	170	175	
Asn Leu Met Asn Tyr Ile Leu Asn Gly Ile Gly Leu Gln Asn			
180	185	190	

<210> 7
<211> 200
<212> PRT
<213> Mycobacterium tuberculosis

<400> 7

Met Asp Arg Val Ala Gly Gln Val Asn Ser Arg Arg Gly Glu Leu Leu			
1	5	10	15
Glu Leu Ala Ala Ala Met Phe Ala Glu Arg Gly Leu Arg Ala Thr Thr			
20	25	30	
Val Arg Asp Ile Ala Asp Gly Ala Gly Ile Leu Ser Gly Ser Leu Tyr			
35	40	45	
His His Phe Ala Ser Lys Glu Glu Met Val Asp Glu Leu Leu Arg Gly			
50	55	60	
Phe Leu Asp Trp Leu Phe Ala Arg Tyr Arg Asp Ile Val Asp Ser Thr			
65	70	75	80
Ala Asn Pro Leu Glu Arg Leu Gln Gly Leu Phe Met Ala Ser Phe Glu			
85	90	95	
Ala Ile Glu His His Ala Gln Val Val Ile Tyr Gln Asp Glu Ala			
100	105	110	
Gln Arg Leu Ala Ser Gln Pro Arg Phe Ser Tyr Ile Glu Asp Arg Asn			
115	120	125	
Lys Gln Gln Arg Lys Met Trp Val Asp Val Leu Asn Gln Gly Ile Glu			
130	135	140	
Glu Gly Tyr Phe Arg Pro Asp Leu Asp Val Asp Leu Val Tyr Arg Phe			
145	150	155	160
Ile Arg Asp Thr Thr Trp Val Ser Val Arg Trp Tyr Arg Pro Gly Gly			
165	170	175	
Pro Leu Thr Ala Gln Gln Val Gly Gln Gln Tyr Leu Ala Ile Val Leu			
180	185	190	
Gly Gly Ile Thr Lys Glu Gly Val			
195	200		

<210> 8
<211> 192
<212> PRT
<213> Auifex aeolicus

<400> 8

Met Tyr Ile Leu Leu Phe Met Gly Glu Lys Arg Ser Asp Thr Lys Glu
1 5 10 15
Lys Ile Leu Ser Ser Ala Leu Lys Leu Phe Ser Lys Lys Gly Phe Lys
20 25 30
Glu Thr Thr Ile Lys Asp Ile Ala Lys Glu Val Gly Ile Thr Glu Gly
35 40 45
Ala Ile Tyr Arg His Phe Thr Ser Lys Glu Glu Ile Ile Lys Ser Leu
50 55 60
Leu Glu Ser Ile Thr Lys Glu Leu Arg His Lys Leu Glu Val Ala Leu
65 70 75 80
Gln Arg Gly Glu Thr Asp Glu Glu Ile Leu Glu Ser Ile Val Asp Thr
85 90 95
Leu Ile Asp Tyr Ala Phe Ser Asn Pro Glu Ser Phe Arg Phe Leu Asn
100 105 110
Leu Tyr His Leu Leu Lys Glu Tyr Gly Glu Val Lys Asn Leu Pro Gly
115 120 125
Glu Leu Ile Leu Lys Phe Leu Asn Gly Leu Tyr Leu Lys Arg Lys Leu
130 135 140
Lys Thr Tyr Pro Glu Ile Ala Ala Val Val Thr Gly Ser Val Glu
145 150 155 160
Arg Val Phe Ile Phe Lys Glu Arg Asn Phe Leu Asp Tyr Asp Glu Glu
165 170 175
Thr Ile Lys Lys Glu Leu Lys Lys Val Leu Lys Ser Ala Ile Leu Ala
180 185 190

<210> 9

<211> 18

<212> DNA

<213> Unknown

<220>

<223> Microbial Organism from the human gut

<400> 9

ccgtgggcat ccagtccg

18

<210> 10

<211> 19

<212> DNA

<213> Unknown

<220>

<223> Microbial Organism from the human gut

<400> 10

tctgctcata cacgtcacg

19